

SEQUENCE LISTING

<110> Green, Allan
Singh, Surinder
Lenman, Marit
Stymne, Sten

<120> FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN
MODIFYING FATTY ACID METABOLISM

<130> 26-98A

<150> US 09/059769

<151> 1998-04-14

<150> US 60/043706

<151> 1997-04-16

<150> AU PO6223

<151> 1997-04-15

<150> AU PO6226

<151> 1997-04-15

<150> US 60/050403

<151> 1997-06-20

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 1358

<212> DNA

<213> *Crepis palaestina*

<220>

<221> CDS

<222> (30) .. (1151)

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Thr Ser Glu Lys Ser Val Met Glu Arg Val Ser Val Asp Pro Val Thr	
10 15 20	
ttc tca ctg agt gaa ttg aag caa gca atc cct ccc cat tgc ttc cag	149
Phe Ser Leu Ser Glu Leu Lys Gln Ala Ile Pro Pro His Cys Phe Gln	
25 30 35 40	
aga tct gta atc cgc tca tct tac tat gtt gtt caa gat ctc att att	197
Arg Ser Val Ile Arg Ser Ser Tyr Tyr Val Val Gln Asp Leu Ile Ile	
45 50 55	
gcc tac atc ttc tac ttc ctt gcc aac aca tat atc cct act ctt cct	245
Ala Tyr Ile Phe Tyr Phe Leu Ala Asn Thr Tyr Ile Pro Thr Leu Pro	
60 65 70	
act agt cta gcc tac tta gct tgg ccc gtt tac tgg ttc tgt caa gct	293
Thr Ser Leu Ala Tyr Leu Ala Trp Pro Val Tyr Trp Phe Cys Gln Ala	
75 80 85	
agc gtc ctc act ggc tta tgg atc ctc ggc cac gaa tgt ggt cac cat	341
Ser Val Leu Thr Gly Leu Trp Ile Leu Gly His Glu Cys Gly His His	
90 95 100	
gcc ttt agc aac tac aca tgg ttt gac gac act gtg ggc ttc atc ctc	389
Ala Phe Ser Asn Tyr Thr Trp Phe Asp Asp Thr Val Gly Phe Ile Leu	
105 110 115 120	
cac tca ttt ctc ctc acc ccg tat ttc tct tgg aaa ttc agt cac cgg	437
His Ser Phe Leu Leu Thr Pro Tyr Phe Ser Trp Lys Phe Ser His Arg	
125 130 135	

aat cac cat tcc aac aca agt tcg att gat aac gat gaa gtt tac att	485
Asn His His Ser Asn Thr Ser Ser Ile Asp Asn Asp Glu Val Tyr Ile	
140 145 150	
ccg aaa agc aag tcc aaa ctc gcg cgt atc tat aaa ctt ctt aac aac	533
Pro Lys Ser Lys Ser Lys Leu Ala Arg Ile Tyr Lys Leu Leu Asn Asn	
155 160 165	
cca cct ggt cgg ctg ttg gtt ttg att atc atg ttc acc cta gga ttt	581
Pro Pro Gly Arg Leu Leu Val Leu Ile Ile Met Phe Thr Leu Gly Phe	
170 175 180	
cct tta tac ctc ttg aca aat att tcc ggc aag aaa tac gac agg ttt	629
Pro Leu Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys Tyr Asp Arg Phe	
185 190 195 200	
gcc aac cac ttc gac ccc atg agt cca att ttc aaa gaa cgt gag cgg	677
Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Lys Glu Arg Glu Arg	
205 210 215	
ttt cag gtc ttc ctt tcg gat ctt ggt ctt ctt gcc gtg ttt tat gga	725
Phe Gln Val Phe Leu Ser Asp Leu Gly Leu Leu Ala Val Phe Tyr Gly	
220 225 230	
att aaa gtt gct gta gca aat aaa gga gct gct tgg gta gcg tgc atg	773
Ile Lys Val Ala Val Ala Asn Lys Gly Ala Ala Trp Val Ala Cys Met	
235 240 245	
tat gga gtt ccg gta tta ggc gta ttt acc ttt ttc gat gtg atc acc	821
Tyr Gly Val Pro Val Leu Gly Val Phe Thr Phe Phe Asp Val Ile Thr	
250 255 260	
ttc ttg cac cac acc cat cag tcg tcg cct cat tat gat tca act gaa	869
Phe Leu His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu	
265 270 275 280	
tgg aac tgg atc aga ggg gcc ttg tca gca atc gat agg gac ttt gga	917
Trp Asn Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Arg Asp Phe Gly	
285 290 295	
ttc ctg aat agt gtt ttc cat gat gtt aca cac act cat gtc atg cat	965
Phe Leu Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His	
300 305 310	
cat ttg ttt tca tac att cca cac tat cat gca aag gag gca agg gat	1013
His Leu Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp	
315 320 325	
gca atc aag cca atc ttg ggc gac ttt tat atg atc gac agg act cca	1061
Ala Ile Lys Pro Ile Leu Gly Asp Phe Tyr Met Ile Asp Arg Thr Pro	
330 335 340	
att tta aaa gca atg tgg aga gag ggc agg gag tgc atg tac atc gag	1109
Ile Leu Lys Ala Met Trp Arg Glu Gly Arg Glu Cys Met Tyr Ile Glu	
345 350 355 360	

cct gat agc aag ctc aaa ggt gtt tat tgg tat cat aaa ttg 1151
 Pro Asp Ser Lys Leu Lys Gly Val Tyr Trp Tyr His Lys Leu
 365 370

tgatcatatg caaaatgcac atgcattttc aaaccctcta gttacgtttg ttctatgtat 1211
 aataaaccgc cggtcctttg gttgactatg cctaagccag gcgaaacagt taaataatat 1271
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<212> PRT

<213> Crepis palaestina

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Ala Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr
 35 40 45

Tyr Val Val Gln Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala
 50 55 60

Asn Thr Tyr Ile Pro Thr Leu Pro Thr Ser Leu Ala Tyr Leu Ala Trp
 65 70 75 80

Pro Val Tyr Trp Phe Cys Gln Ala Ser Val Leu Thr Gly Leu Trp Ile
 85 90 95

Leu Gly His Glu Cys Gly His His Ala Phe Ser Asn Tyr Thr Trp Phe
 100 105 110

Asp Asp Thr Val Gly Phe Ile Leu His Ser Phe Leu Leu Thr Pro Tyr
 115 120 125

Phe Ser Trp Lys Phe Ser His Arg Asn His His Ser Asn Thr Ser Ser
 130 135 140

Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala
 145 150 155 160

Arg Ile Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Leu
 165 170 175

Ile Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile
 180 185 190

Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser
 195 200 205

Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Phe Leu Ser Asp Leu
 210 215 220

Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Asn Lys
 225 230 235 240

Gly Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Val Leu Gly Val
 245 250 255

Phe Thr Phe Phe Asp Val Ile Thr Phe Leu His His Thr His Gln Ser
 260 265 270

Ser Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu
 275 280 285

Ser Ala Ile Asp Arg Asp Phe Gly Phe Leu Asn Ser Val Phe His Asp
 290 295 300

Val Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His
 305 310 315 320

Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Ile Leu Gly Asp
 325 330 335

Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu
 340 345 350

ctg agt gat ttg aag caa gca atc cct cca cat tgc ttc cag cga tct 148
Leu Ser Asp Leu Lys Gln Ala Ile Pro Pro His Cys Phe Gln Arg Ser
30 35 40

gtc Val	atc Ile	cgt Arg	tca Ser 45	tct Ser	tat Tyr	tac Tyr	gtt Val	gtt Val	cag Gln	gat Asp	ctc Leu	ata Ile	att Ile 55	gcc Ala	tac Tyr	196
atc Ile	ttc Phe 60	tac Tyr	ttc Phe	ctt Leu	gcc Ala	aac Asn 65	aca Thr	tat Tyr	atc Ile	cct Pro	aat Asn 70	ctc Leu	cct Pro	cat His	cct Pro	244
cta Leu	gcc Ala 75	tac Tyr	tta Leu	gct Ala	tgg Trp 80	ccg Pro	ctt Leu	tac Tyr	tgg Trp	ttc Phe 85	tgt Cys	caa Gln	gct Ala	agc Ser	gtc Val	292
ctc Leu 90	act Thr	ggg Gly	tta Leu	tgg Trp 95	atc Ile	ctc Leu	ggc Gly	cat His	gaa Glu	tgt Cys 100	ggg Gly	cac His	cat His	gcc Ala	tat Tyr 105	340
agc Ser	aac Asn	tac Tyr	aca Thr 110	tgg Trp	gtt Val	gac Asp	gac Asp	act Thr 115	gtg Val	ggc Gly	ttc Phe	atc Ile	atc Ile	cat His 120	tca Ser	388
ttt Phe	ctc Leu	ctc Leu	acc Thr 125	ccg Pro	tat Tyr	ttc Phe	tct Ser	tgg Trp 130	aaa Lys	tac Tyr	agt Ser	cac His 135	cgg Arg	aat Asn	cac His	436
cat His	tcc Ser 140	aac Asn	aca Thr	agt Ser	tcg Ser	att Ile	gat Asp 145	aac Asn	gat Asp	gaa Glu	gtt Val 150	tac Tyr	att Ile	ccg Pro	aaa Lys	484
agc Ser	aag Lys 155	tcc Ser	aaa Lys	ctc Leu	aag Lys	cgt Arg 160	atc Ile	tat Tyr	aaa Lys	ctt Leu 165	ctt Leu	aac Asn	aac Asn	cca Pro	cct Pro	532
ggg Gly 170	cga Arg	ctg Leu	ttg Leu	gtt Val	ttg Leu	gtt Val	atc Ile	atg Met	ttc Phe	acc Thr 180	cta Leu	gga Gly	ttt Phe	cct Pro	tta Leu 185	580
tac Tyr	ctc Leu	ttg Leu	aca Thr 190	aat Asn	att Ile	tcc Ser	ggc Gly	aag Lys 195	aaa Lys	tac Tyr	gat Asp	agg Arg	ttt Phe	gcc Ala 200	aac Asn	628
cac His	ttc Phe	gac Asp 205	ccc Pro	atg Met	agt Ser	cca Pro	att Ile	ttc Phe 210	aaa Lys	gaa Glu	cgt Arg	gag Glu	cgg Arg 215	ttt Phe	cag Gln	676
gtc Val	ttc Phe 220	ctt Leu	tcg Ser	gat Asp	ctt Leu	ggg Gly	ctt Leu	ctt Leu	gct Ala	gtg Val	ttt Phe 230	tat Tyr	gga Gly	att Ile	aaa Lys	724
gtt Val	gct Ala 235	gta Val	gca Ala	aat Asn	aaa Lys	gga Gly 240	gct Ala	gct Ala	tgg Trp	gtg Val	gcg Ala 245	tgc Cys	atg Met	tat Tyr	gga Gly	772
gtt Val 250	ccg Pro	gtg Val	cta Leu	ggc Gly	gta Val 255	ttt Phe	acc Thr	ttt Phe	ttc Phe	gat Asp 260	gtg Val	atc Ile	acg Thr	ttc Phe	tta Leu 265	820

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cac cac acc cat cag tcg tcg cct cat tat gat tca act gaa tgg aac      868
His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu Trp Asn
                270                275                280

tgg atc aga ggg gct ttg tca gca atc gat agn gac ttt ggg ttc ctg      916
Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Xaa Asp Phe Gly Phe Leu
                285                290                295

aat agt gtt ttc cat gat gtn aca cac act cac gtc atg cat cat ttg      964
Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His His Leu
                300                305                310

ttt tca tac att cca cac tat cat gca aag gaa gca agg gat gca atc      1012
Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile
                315                320                325

aaa ccg atc ttg ggc gac ttt tat atg atc gat agg act cca att tta      1060
Lys Pro Ile Leu Gly Asp Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu
                330                335                340                345

aaa gca atg tgg aga gag ggc agg gaa tgc atg tac atc gag cct gat      1108
Lys Ala Met Trp Arg Glu Gly Arg Glu Cys Met Tyr Ile Glu Pro Asp
                350                355                360

agc aag ctc aaa ggt gtt tat tgg tat cat aaa ttg tga tcatatgcaa      1157
Ser Lys Leu Lys Gly Val Tyr Trp Tyr His Lys Leu
                365                370

aatgcacatg cattttcaaa ccctctagtt acctttgttc tatgtataat aagaccgccg      1217

gtcctatgggt tttctatgcc taagccaggc gaaatagtta aataatatcg gtatgatgta      1277

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<211> 373

<212> PRT

<213> Crepis sp.

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<222> (292)..(292)

<223> The 'Xaa' at location 292 stands for Arg, or Ser.

<220>

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<222> (937)..(937)

<223> N is any nucleotide residue

<220>

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<222> (901)..(901)

<223> N is any nucleotide residue

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Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr Tyr
35 40 45

Val Val Gln Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala Asn
50 55 60

Thr Tyr Ile Pro Asn Leu Pro His Pro Leu Ala Tyr Leu Ala Trp Pro
65 70 75 80

Leu Tyr Trp Phe Cys Gln Ala Ser Val Leu Thr Gly Leu Trp Ile Leu
85 90 95

Gly His Glu Cys Gly His His Ala Tyr Ser Asn Tyr Thr Trp Val Asp
100 105 110

Asp Thr Val Gly Phe Ile Ile His Ser Phe Leu Leu Thr Pro Tyr Phe
115 120 125

Ser Trp Lys Tyr Ser His Arg Asn His His Ser Asn Thr Ser Ser Ile
130 135 140

Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Lys Arg
145 150 155 160

Ile Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Leu Val
165 170 175

Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile Ser
 180 185 190

Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro
 195 200 205

Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Phe Leu Ser Asp Leu Gly
 210 215 220

Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Asn Lys Gly
 225 230 235 240

Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Val Leu Gly Val Phe
 245 250 255

Thr Phe Phe Asp Val Ile Thr Phe Leu His His Thr His Gln Ser Ser
 260 265 270

Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu Ser
 275 280 285

Ala Ile Asp Xaa Asp Phe Gly Phe Leu Asn Ser Val Phe His Asp Val
 290 295 300

Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His Tyr
 305 310 315 320

His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Ile Leu Gly Asp Phe
 325 330 335

Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu Gly
 340 345 350

Arg Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Leu Lys Gly Val Tyr
 355 360 365

Trp Tyr His Lys Leu
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<210> 5

<211> 550

<212> DNA

<213> *Vernonia galamensis*

<220>

<221> CDS

<222> (1)..(549)

<223>

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atc ctt cac ttt gca ctc ttc acc cct tat ttc tct tgg aaa tac agt	96
Ile Leu His Phe Ala Leu Phe Thr Pro Tyr Phe Ser Trp Lys Tyr Ser	
20 25 30	
cac cgt aat cac cat gcc aac aca aac tct ctt gta acc gat gaa gta	144
His Arg Asn His His Ala Asn Thr Asn Ser Leu Val Thr Asp Glu Val	
35 40 45	
tac atc cct aaa gtt aaa tcc aag gtc aag att tat tcc aaa atc ctt	192
Tyr Ile Pro Lys Val Lys Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu	
50 55 60	
aac aac cct cct ggt cgc gtt ttc acc ttg gct ttc aga ttg atc gtg	240
Asn Asn Pro Pro Gly Arg Val Phe Thr Leu Ala Phe Arg Leu Ile Val	
65 70 75 80	
ggt ttt cct tta tac ctt ttc acc aat gtt tca ggc aag aaa tac gaa	288
Gly Phe Pro Leu Tyr Leu Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu	
85 90 95	
cgt ttt gcc aac cat ttt gat ccc atg agt ccc att ttc acc gag cgt	336
Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Thr Glu Arg	
100 105 110	
gag cat gta caa gtc ttg ctt tct gat ttt ggt ctc ata gca gtt gct	384
Glu His Val Gln Val Leu Leu Ser Asp Phe Gly Leu Ile Ala Val Ala	
115 120 125	
tac gtg gtt cgt caa gct gta ctg gct aaa gga ggt gct tgg gtg atg	432
Tyr Val Val Arg Gln Ala Val Leu Ala Lys Gly Gly Ala Trp Val Met	
130 135 140	
tgc att tac gga gtt cct gtg ctg gcc gta aac gca ttc ttt gtt tta	480
Cys Ile Tyr Gly Val Pro Val Leu Ala Val Asn Ala Phe Phe Val Leu	
145 150 155 160	

atc act tat ctt cac cac acg cat ctc tca ctg ccc cac tat gat agc 528
 Ile Thr Tyr Leu His His Thr His Leu Ser Leu Pro His Tyr Asp Ser
 165 170 175

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 Ser Glu Trp Asp Trp Leu Arg
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<210> 6

<211> 183

<212> PRT

<213> *Vernonia galamensis*

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 20 25 30

His Arg Asn His His Ala Asn Thr Asn Ser Leu Val Thr Asp Glu Val
 35 40 45

Tyr Ile Pro Lys Val Lys Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu
 50 55 60

Asn Asn Pro Pro Gly Arg Val Phe Thr Leu Ala Phe Arg Leu Ile Val
 65 70 75 80

Gly Phe Pro Leu Tyr Leu Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu
 85 90 95

Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Thr Glu Arg
 100 105 110

Glu His Val Gln Val Leu Leu Ser Asp Phe Gly Leu Ile Ala Val Ala
 115 120 125

Tyr Val Val Arg Gln Ala Val Leu Ala Lys Gly Gly Ala Trp Val Met
 130 135 140

Cys Ile Tyr Gly Val Pro Val Leu Ala Val Asn Ala Phe Phe Val Leu
 145 150 155 160

Ile Thr Tyr Leu His His Thr His Leu Ser Leu Pro His Tyr Asp Ser
 165 170 175

Ser Glu Trp Asp Trp Leu Arg
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<210> 7

<211> 177

<212> DNA

<213> *Crepis alpina*

<220>

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<222> (1)..(177)

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 1 5 10 15

gtg ggc ttc atc ctc cac tcg ttt ctc atg acc ccg tat ttc tcc tgg 96
 Val Gly Phe Ile Leu His Ser Phe Leu Met Thr Pro Tyr Phe Ser Trp
 20 25 30

aaa tac agc cac cgg aac cac cat gcc aac aca aat tcg ctt gac aac 144
 Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser Leu Asp Asn
 35 40 45

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 Asp Glu Val Tyr Ile Pro Lys Ser Lys Ala Lys
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<210> 8

<211> 59

<212> PRT

<213> *Crepis alpina*

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Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Asn
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Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160

Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175

Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
 180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
 195 200 205

His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
 210 215 220

Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
 225 230 235 240

Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
 245 250 255

Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
 260 265 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
 275 280 285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 290 295 300

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 305 310 315 320

Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
 325 330 335

Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
 340 345 350

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His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190

Tyr Trp Ala Phe Asn Val Ser Gly Arg Pro Tyr Pro Glu Gly Phe Ala
 195 200 205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220

Gln Ile Tyr Val Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240

Tyr Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Leu Tyr
 245 250 255

Gly Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr
 260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285

Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320

Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Val Thr Lys Ala
 325 330 335

Ile Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp
 340 345 350

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

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<212> PRT

<213> Glycine max

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Leu Ser Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser
 35 40 45

Val Leu Arg Ser Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe
 50 55 60

Cys Leu Tyr Tyr Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro
 65 70 75 80

Leu Ser Phe Arg Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile
 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110

Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly Leu Ile Leu His Ser
 115 120 125

Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160

Gly Arg Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu
 165 170 175

Tyr Leu Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys
 180 185 190

His Tyr Asp Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
 195 200 205

Ile Tyr Ile Ser Asp Ala Gly Val Leu Ala Val Val Tyr Gly Leu Phe
 210 215 220

Arg Leu Ala Met Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly
 225 230 235 240

Val Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Phe Leu
 245 250 255

Gln His Thr His Pro Ala Leu Pro His Tyr Thr Ser Ser Glu Trp Asp
 260 265 270

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 275 280 285

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 290 295 300

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
 305 310 315 320

Lys Pro Ile Leu Gly Glu Tyr Tyr Arg Phe Asp Glu Thr Pro Phe Val
 325 330 335

Lys Ala Met Trp Arg Glu Ala Arg Glu Cys Ile Tyr Val Glu Pro Asp
 340 345 350

Gln Ser Thr Glu Ser Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 355 360 365

<210> 12

<211> 383

<212> PRT

<213> Solanum commersonii

<400> 12

Met Gly Ala Gly Gly Arg Met Ser Ala Pro Asn Gly Glu Thr Glu Val
 1 5 10 15

Lys Arg Asn Pro Leu Gln Lys Val Pro Thr Ser Lys Pro Pro Phe Thr
 20 25 30

Val Gly Asp Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser
 35 40 45

Leu Ile Arg Ser Phe Ser Tyr Val Val Tyr Asp Leu Ile Leu Val Ser
 50 55 60

Ile Met Tyr Tyr Val Ala Asn Thr Tyr Phe His Leu Leu Pro Ser Pro
 65 70 75 80

Tyr Cys Tyr Ile Ala Trp Pro Ile Tyr Trp Ile Cys Gln Gly Cys Val
 85 90 95

Cys Thr Gly Ile Trp Val Asn Ala His Glu Cys Gly His His Ala Phe
 100 105 110

Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu Ile Leu His Ser
 115 120 125

Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160

Pro Lys Ser Gln Leu Gly Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro
 165 170 175

Gly Arg Val Leu Ser Leu Thr Ile Thr Leu Thr Leu Gly Trp Pro Leu
 180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys
 195 200 205

His Tyr Asp Pro Tyr Gly Pro Ile Tyr Asn Asn Arg Glu Arg Leu Gln
 210 215 220

Ile Phe Ile Ser Asp Ala Gly Val Leu Gly Val Cys Tyr Leu Leu Tyr
 225 230 235 240

Arg Ile Ala Leu Val Lys Gly Leu Ala Trp Leu Val Cys Val Tyr Gly
 245 250 255

Val Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu
 260 265 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asp
 275 280 285

Trp Leu Arg Gly Ala Leu Ala Thr Cys Asp Arg Asp Tyr Gly Val Leu
 290 295 300

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Val His His Leu
 305 310 315 320

Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Val
 325 330 335

Lys Pro Leu Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Ile Tyr
 340 345 350

Lys Glu Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Lys Asp
 355 360 365

Glu Ser Ser Gln Gly Lys Gly Val Phe Trp Tyr Lys Asn Lys Leu
 370 375 380

<210> 13

<211> 387

<212> PRT

<213> Glycine max

<400> 13

Met Gly Leu Ala Lys Glu Thr Thr Met Gly Gly Arg Gly Arg Val Ala
 1 5 10 15

Lys Val Glu Val Gln Gly Lys Lys Pro Leu Ser Arg Val Pro Asn Thr
 20 25 30

Lys Pro Pro Phe Thr Val Gly Gln Leu Lys Lys Ala Ile Pro Pro His
 35 40 45

Cys Phe Gln Arg Ser Leu Leu Thr Ser Phe Ser Tyr Val Val Tyr Asp
 50 55 60

Leu Ser Phe Ala Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu
 65 70 75 80

Leu Pro Gln Pro Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu
 85 90 95

Gln Gly Cys Leu Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly
 100 105 110

His His Ala Phe Ser Lys Tyr Gln Trp Val Asp Asp Val Val Gly Leu
 115 120 125

Thr Leu His Ser Thr Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser
 130 135 140

His Arg Arg His His Ser Asn Thr Gly Ser Leu Asp Arg Asp Glu Val
 145 150 155 160

Phe Val Pro Lys Pro Lys Ser Lys Val Ala Trp Phe Ser Lys Tyr Leu
 165 170 175

Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile
 180 185 190

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 195 200 205

Ser Phe Ala Ser His Tyr His Pro Tyr Ala Pro Ile Tyr Ser Asn Arg
 210 215 220

Glu Arg Leu Leu Ile Tyr Val Ser Asp Val Ala Leu Phe Ser Val Thr
 225 230 235 240

Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
20 25 30

Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
 35 40 45

Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
 50 55 60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
 65 70 75 80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
 85 90 95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
 100 105 110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
 115 120 125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
 130 135 140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
 145 150 155 160

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
 165 170 175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
 180 185 190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 195 200 205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
 210 215 220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
 225 230 235 240

Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
 245 250 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
 260 265 270

Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
 275 280 285

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
 290 295 300

Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
 305 310 315 320

Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
 325 330 335

Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
 340 345 350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
 355 360 365

Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
 370 375 380

Asn Lys Tyr
 385

<210> 15

<211> 6

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 15

His Glu Cys Gly His His
 1 5

<210> 16

<211> 5

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 16

His Arg Asn His His
1 5

<210> 17

<211> 5

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 17

His Val Met His His
1 5

<210> 18

<211> 5

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 18

His Val Leu His His
1 5

<210> 19

<211> 1199

<212> DNA

<213> *Vernonia galamensis*

<220>

<221> CDS

<222> (44) .. (1195)

<223>

<400> 19

tattacacat	ttacactgat	ctgttaatca	aatttcaaac	aaa	atg	gga	gct	ggg										55
												Met	Gly	Ala	Gly			
												1						
ggc	cga	atg	aat	acc	acc	gat	gat	gat	cag	aag	aat	ctc	ttc	caa	cgc			103
Gly	Arg	Met	Asn	Thr	Thr	Asp	Asp	Asp	Gln	Lys	Asn	Leu	Phe	Gln	Arg			
5					10					15					20			
gta	cca	gcc	tcc	aaa	cca	cca	ttc	tcc	ttg	gct	gat	ctt	aag	aaa	gcc			151
Val	Pro	Ala	Ser	Lys	Pro	Pro	Phe	Ser	Leu	Ala	Asp	Leu	Lys	Lys	Ala			
				25					30					35				
ata	cca	ccc	cac	tgt	ttc	caa	aga	tcc	ctc	ctc	cgt	tca	tct	tac	tat			199
Ile	Pro	Pro	His	Cys	Phe	Gln	Arg	Ser	Leu	Leu	Arg	Ser	Ser	Tyr	Tyr			
			40					45					50					
gtg	gtt	cat	gat	ctc	gtc	gta	gcc	tac	gtc	ttt	tac	tat	ctc	gcc	aac			247
Val	Val	His	Asp	Leu	Val	Val	Ala	Tyr	Val	Phe	Tyr	Tyr	Leu	Ala	Asn			
		55					60					65						
aca	tac	atc	cct	ctt	ctt	ccc	tcc	cct	ctt	gcc	tac	tta	tta	gct	tgg			295
Thr	Tyr	Ile	Pro	Leu	Leu	Pro	Ser	Pro	Leu	Ala	Tyr	Leu	Leu	Ala	Trp			
		70				75					80							
ccc	ctt	tac	tgg	ttc	tgt	cag	ggg	agc	atc	ctc	acc	ggg	gtc	tgg	gtc			343
Pro	Leu	Tyr	Trp	Phe	Cys	Gln	Gly	Ser	Ile	Leu	Thr	Gly	Val	Trp	Val			
85					90					95					100			
atc	ggg	cat	gaa	tgt	ggc	cac	cat	gcc	ttc	agt	gac	tat	caa	tgg	ata			391
Ile	Gly	His	Glu	Cys	Gly	His	His	Ala	Phe	Ser	Asp	Tyr	Gln	Trp	Ile			
				105					110					115				
gac	gac	act	gtg	ggc	ttc	atc	ctt	cac	tct	gca	ctc	ttc	acc	cct	tat			439
Asp	Asp	Thr	Val	Gly	Phe	Ile	Leu	His	Ser	Ala	Leu	Phe	Thr	Pro	Tyr			
			120					125					130					
ttc	tct	tgg	aaa	tac	agt	cac	cgt	aat	cac	cat	gcc	aac	aca	aac	tct			487
Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Asn	His	His	Ala	Asn	Thr	Asn	Ser			
			135					140					145					
ctt	gat	aac	gat	gaa	gta	tac	atc	cct	aaa	gtt	aaa	tcc	aag	gtc	aag			535
Leu	Asp	Asn	Asp	Glu	Val	Tyr	Ile	Pro	Lys	Val	Lys	Ser	Lys	Val	Lys			
			150				155					160						
att	tat	tcc	aaa	atc	ctt	aac	aac	cct	cct	ggg	cgc	gtt	ttc	acc	ttg			583
Ile	Tyr	Ser	Lys	Ile	Leu	Asn	Asn	Pro	Pro	Gly	Arg	Val	Phe	Thr	Leu			
165					170					175					180			
gct	ttc	aga	ttg															

ccc att ttc acc gag cgt gag cat gta caa gtc ttg ctt tct gat ttt 727
Pro Ile Phe Thr Glu Arg Glu His Val Gln Val Leu Leu Ser Asp Phe
215 220 225

ggg ctc ata gca gtt gct tac gtg gtt cgt caa gct gta ctg gct aaa 775
Gly Leu Ile Ala Val Ala Tyr Val Val Arg Gln Ala Val Leu Ala Lys
230 235 240

gga ggt gct tgg gtg atg tgc att tac gga gtt cct gtg ctg gcc gta 823
Gly Gly Ala Trp Val Met Cys Ile Tyr Gly Val Pro Val Leu Ala Val
245 250 255 260

aac gca ttc ttt gtt tta atc act tat ctt cac cac acg cat ctc tca 871
Asn Ala Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu Ser
265 270 275

ctg cct cac tat gat tgc act gaa tgg gac tgg atc aag gga gct ttg 919
Leu Pro His Tyr Asp Ser Thr Glu Trp Asp Trp Ile Lys Gly Ala Leu
280 285 290

tgc acc atc gac aga gat ttc gga ttc ttg aat agg gtt ttc cac gac 967
Cys Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His Asp
295 300 305

gtg aca cac acc cat gtg ttg cat cat ttg ata tgc tac att cct cat 1015
Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro His
310 315 320

tat cat gca aag gag gca aga gac gcc atc aaa ccg gtg ttg ggc gaa 1063
Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly Glu
325 330 335 340

tac tat aag atc gac agg aca ccg atc gtg aag gca atg tgg agg gaa 1111
Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Val Lys Ala Met Trp Arg Glu
345 350 355

gca aag aat gca tat aca ttg agg ctg atg aag ata gcg agc acc aag 1159
Ala Lys Asn Ala Tyr Thr Leu Arg Leu Met Lys Ile Ala Ser Thr Lys
360 365 370

gca cat act ggt acc aca agt tgt aaa gcc aga tcc taag 1199
Ala His Thr Gly Thr Thr Ser Cys Lys Ala Arg Ser
375 380

<210> 20

<211> 384

<212> PRT

<213> Vernonia galamensis

<400> 20

Met Gly Ala Gly Gly Arg Met Asn Thr Thr Asp Asp Asp Gln Lys Asn
1 5 10 15

Leu Phe Gln Arg Val Pro Ala Ser Lys Pro Pro Phe Ser Leu Ala Asp
20 25 30

Leu Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Arg
35 40 45

Ser Ser Tyr Tyr Val Val His Asp Leu Val Val Ala Tyr Val Phe Tyr
50 55 60

Tyr Leu Ala Asn Thr Tyr Ile Pro Leu Leu Pro Ser Pro Leu Ala Tyr
65 70 75 80

Leu Leu Ala Trp Pro Leu Tyr Trp Phe Cys Gln Gly Ser Ile Leu Thr
85 90 95

Gly Val Trp Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Asp
100 105 110

Tyr Gln Trp Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu
115 120 125

Phe Thr Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala
130 135 140

Asn Thr Asn Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Val Lys
145 150 155 160

Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg
165 170 175

Val Phe Thr Leu Ala Phe Arg Leu Ile Val Gly Phe Pro Leu Tyr Leu
180 185 190

Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu Arg Phe Ala Asn His Phe
195 200 205

Asp Pro Met Ser Pro Ile Phe Thr Glu Arg Glu His Val Gln Val Leu
210 215 220

Leu Ser Asp Phe Gly Leu Ile Ala Val Ala Tyr Val Val Arg Gln Ala
 225 230 235 240

Val Leu Ala Lys Gly Gly Ala Trp Val Met Cys Ile Tyr Gly Val Pro
 245 250 255

Val Leu Ala Val Asn Ala Phe Phe Val Leu Ile Thr Tyr Leu His His
 260 265 270

Thr His Leu Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asp Trp Ile
 275 280 285

Lys Gly Ala Leu Cys Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg
 290 295 300

Val Phe His Asp Val Thr His Thr His Val Leu His His Leu Ile Ser
 305 310 315 320

Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro
 325 330 335

Val Leu Gly Glu Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Val Lys Ala
 340 345 350

Met Trp Arg Glu Ala Lys Asn Ala Tyr Thr Leu Arg Leu Met Lys Ile
 355 360 365

Ala Ser Thr Lys Ala His Thr Gly Thr Thr Ser Cys Lys Ala Arg Ser
 370 375 380

<210> 21

<211> 5

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(4)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any amino acid; Xaa at position 4 is any amino acid;

<400> 21

His Xaa Xaa Xaa His
1 5

<210> 22

<211> 6

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(5)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any amino acid; Xaa at position 4 is any amino acid; Xaa at position 5 is any amino acid;

<400> 22

His Xaa Xaa Xaa Xaa His
1 5

<210> 23

<211> 5

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any amino acid;

<400> 23

His Xaa Xaa His His
1 5

<210> 24

<211> 6

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(4)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any amino acid; Xaa at position 4 is any amino acid;

<400> 24

His Xaa Xaa Xaa His His
1 5